



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Harrington, Lea A.
Robinson, Murray O.
- (ii) TITLE OF INVENTION: NOVEL GENES ENCODING TELOMERASE PROTEINS
- (iii) NUMBER OF SEQUENCES: 44
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Amgen Inc.
 - (B) STREET: One Amgen Center Drive
 - (C) CITY: Thousand Oaks
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 91320-1789
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/951,733
 - (B) FILING DATE: 16-OCT-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/873,039
 - (B) FILING DATE: 11-JUN-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/751,189
 - (B) FILING DATE: 15-NOV-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Oleski, Nancy A.
 - (B) REGISTRATION NUMBER: 34,688
 - (C) REFERENCE/DOCKET NUMBER: A-433B
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (805) 447-6504
 - (B) TELEFAX: (805) 499-8011

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7881 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGAAAAAC TCCATGGGCA TGTGTCTGCC CATCCAGACA TCCTCTCCTT GGAGAACCGG

TGCCTGGCTA	TGCTCCCTGA	CTTACAGCCC	TTGGAGAAAC	TACATCAGCA	TGTATCTACC	120
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TGCCTGGCCA	CACTTTCTGA	CCTGAAGACC	ATGGAGAAAC	CACATGGACA	TGTTTCTGCC	300
CACCCAGACA	TCCTCTCCTT	GGAGAACCGG	TGCCTGGCCA	CCCTCCCTAG	TCTAAAGAGC	360
ACTGTGTCTG	CCAGCCCCTT	GTTCCAGAGT	CTACAGATAT	CTCACATGAC	GCAAGCTGAT	420
TTGTACCGTG	TGAACAACAG	CAATTGCCTG	CTCTCTGAGC	CTCCAAGTTG	GAGGGCTCAG	480
CATTTCTCTA	AGGGACTAGA	CCTTTCAACC	TGCCCTATAG	CCCTGAAATC	CATCTCTGCC	540
ACAGAGACAG	CTCAGGAAGC	AACTTTGGGT	CGTTGGTTTG	ATTCAGAAGA	GAAGAAAGGG	600
GCAGAGACCC	AAATGCCTTC	TTATAGTCTG	AGCTTGGGAG	AGGAGGAGGA	GGTGGAGGAT	660
CTGGCCGTGA	AGCTCACCTC	TGGAGACTCT	GAATCTCATC	CAGAGCCTAC	TGACCATGTC	720
CTTCAGGAAA	AGAAGATGGC	TCTACTGAGC	TTGCTGTGCT	CTACTCTGGT	CTCAGAAGTA	780
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GCCCTCCTGG	AGCCTGAGTT	TATCCTCAAG	GCATCTTTGT	ATGCCAGGCA	GCAGCTGAAC	900
GTCCGGAATG	TGGCCAATAA	CATCTTGGCC	ATTGCTGCTT	TCTTGCCGGC	GTGTGCCCCC	960
CACCTGCGAC	GATATTTCTG	TGCCATTGTC	CAGCTGCCTT	CTGACTGGAT	CCAGGTGGCT	1020
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CTCCGTACTG	CCATGACGGA	CAAATTTGCC	CAGTTTGACG	AGTACCAGCT	GGCTAAGTAC	1140
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CTGGGTTACA	GATACCCCTC	CAACCTACAG	CTCTTTTCTC	GAAGTCGCCT	TCCTGGGCCT	1440
TGGGATTCTA	GCAGAGCTGG	GAAGAGGATG	AAGCTGTCTA	GGCCAGAGAC	CTGGGAGCGG	1500
GAGCTGAGCC	TACGGGGGAA	CAAAGCGTCG	GTCTGGGAGG	AACTCATTGA	AAATGGGAAG	1560
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CGCCACCATG	AGCTCATTCT	CCAGAGACTC	CAGCATGGGA	AGTCGGTGAT	CCACAGTCGG	1680
CAGTTTCCAT	TCAGATTTCT	TAACGCCCAT	GATGCCATTG	ATGCCCTCGA	GGCTCAACTC	1740
AGAAATCAAG	CATTGCCCTT	TCCTTCGAAT	ATAACACTGA	TGAGGCGGAT	ACTAACTAGA	1800
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GTCGTGCTGT	GTGGAGGTGA	CACTCTGAAG	ACTGCAGTGC	TTAAGGCAGA	AGAAGGCATC	2220
CTGAAGACTG	CCATCAAGCT	CCAGGCTCAA	GTCCAGGAGT	TTGATGAAAA	TGATGGATGG	2280
TCCCTGAATA	CTTTTGGGAA	ATACCTGCTG	TCTCTGGCTG	GCCAAAGGGT	TCCTGTGGAC	2340
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GCCTGGAAAT	CTGACTTTGT	TTCTGAGTCT	GAAGAGGCCG	CATGTCGGAT	CTCAGAACTG	3180
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CCAGTGTCCA	TCCCAGACGA	TGACTTGGTC	CAGGCCACCT	TCCAGCAGCT	GCAGAAGCCA	3420
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GGAAGGCTGA	GCCTGGTGAC	GGGGCAGTCA	GGACAGGGCA	AGACAGCCTT	CCTGGCATCT	3540
CTTGTGTCAG	CCCTGCAGGC	TCCTGATGGG	GCCAAGGTGG	CACCATTAGT	CTTCTTCCAC	3600
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TATCTGCGTG	GCCAACTAAA	AGAGCCAGGT	GCCCTCCCCA	GCACCTACCG	AAGCCTGGTG	3720
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CAGGTCCTGA	TCATCGATGG	GGCTGATAGG	TTAGTGGACC	AGAATGGGCA	GCTGATTTCA	3840

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AGCACACTGG	AGAAGGAGCA	CGGGCCTGAT	GTCTTCCCC	AGGCCTTGAC	TGCCCTAGAA	4260
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CCTCTGGAGC	GCCCTGGTGC	CCGGCTGTGC	CTCCCTGATG	GGCCCCTGAG	AACAGCAGCT	4500
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CAGCTCTGGA	AGACATGTGA	CGCTGATGCC	TCAGGCACCT	TCCGAAGTTG	CCCTCCTGAG	4620
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CTGGAGCTCT	GGGACCTGCA	GCATGGTTGT	CGGGTGCTGC	AGACTAAGGC	TCACCAGTAC	5280
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CCCGGAGCCT	CTATCCGTAC	CTTGGCCTTC	AATGTGCCTG	GGGGGGTTGT	GGCTGTGGGC	5580
CGGCTGGACA	GTATGGTGGA	GCTGTGGGCC	TGGCGAGAAG	GGGCACGGCT	GGCTGCCTTC	5640
CCTGCCCACC	ATGGCTTTGT	TGCTGCTGCG	CTTTTCCTGC	ATGCGGGTTG	CCAGTTACTG	5700

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CACCTGGGTT	CCCTTTCTCT	CTCTCCTGCC	CTCTCTGTGG	CACTCAGCCC	AGATGGTGAT	5820
CGGGTGGCTG	TTGGATATCG	AGCGGATGGC	ATTAGGATCT	ACAAAATCTC	TTCAGGTTCC	5880
CAGGGGGCTC	AGGGTCAGGC	ACTGGATGTG	GCAGTGTCCG	CCCTGGCCTG	GCTAAGCCCC	5940
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TCCCTTCAGT	CCCTCTGGCT	CCTGTCCAGA	TTCCAGAAGC	CTGTGCTAGG	ACTGGCCACT	6060
TCCCAGGAGC	TCTTGGCTTC	TGCCTCAGAG	GATTTACACAG	TGCAGCTGTG	GCCAAGGCAG	6120
CTGCTGACGC	GGCCACACAA	GGCAGAAAGAC	TTTCCCTGTG	GCACTGAGCT	GCGGGGACAT	6180
GAGGGCCCTG	TGAGCTGCTG	TAGTTTCAGC	ACTGATGGAG	GCAGCCTGGC	CACCGGGGGC	6240
CGGGATCGGA	GTCTCCTCTG	CTGGGACGTG	AGGACACCCA	AAACCCCTGT	TTTGATCCAC	6300
TCCTTCCCTG	CCTGTCACCG	TGACTGGGTC	ACTGGCTGTG	CCTGGACCAA	AGATAACCTA	6360
CTGATATCCT	GCTCCAGTGA	TGGCTCTGTG	GGGCTCTGGG	ACCCAGAGTC	AGGACAGCGG	6420
CTTGGTCAGT	TCCTGGGTCA	TCAGAGTGCT	GTGAGCGCTG	TGGCAGCTGT	GGAGGAGCAC	6480
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ACCAGCATCC	CTGCTCACTC	AGGACCCATT	AGCCACTGTG	CAGCTGCCAT	GGAGCCCCGT	6600
GCAGCTGGAC	AGCCTGGGTC	AGAGCTTCTG	GTGGTAACCG	TCGGGCTAGA	TGGGGCCACA	6660
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AAAATCAGCG	AGTGGCAAGT	GAAACTGCGG	AAGGGTTCGG	CACCCGGAAG	TTTGAGTCTT	7080
CACCTGAACC	GAATTCTACA	GGAGGACTTA	GGGGTGCTGA	CAAGTCTGGA	TTGGGCTCCT	7140
GATGGTCACT	TTCTCATCTT	GGCCAAAGCA	GATTTGAAGT	TACTTTGCAT	GAAGCCAGGG	7200
GATGCTCCAT	CTGAAATCTG	GAGCAGCTAT	ACAGAAAATC	CTATGATATT	GTCCACCCAC	7260
AAGGAGTATG	GCATATTTGT	CCTGCAGCCC	AAGGATCCTG	GAGTTCTTTC	TTTCTTGAGG	7320
CAAAAGGAAT	CAGGAGAGTT	TGAAGAGAGG	CTGAACTTTG	ATATAAACTT	AGAGAATCCT	7380
AGTAGGACCC	TAATATCGAT	AACTCAAGCC	AAACCTGAAT	CTGAGTCCTC	ATTTTTGTGT	7440
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ACAGGTAACA	TGTGGCAGAA	AAAAGCAAAC	ACTCCAGAAA	CCCAAATCC	AGGGACAGAC	7560
CCATCTACCT	GCAGGGAATC	TGATGCCAGC	ATGGATAGTG	ATGCCAGCAT	GGATAGTGAG	7620

CCAACACCAC	ATCTAAAGAC	ACGGCAGCGT	AGAAAGATTC	ACTCGGGCTC	TGTCACAGCC	7680
CTCCATGTGC	TACCTGAGTT	GCTGGTGACA	GCTTCGAAGG	ACAGAGATGT	TAAGCTATGG	7740
GAGAGACCCA	GTATGCAGCT	GCTGGGCCTG	TTCCGATGCG	AAGGGTCAGT	GAGCTGCCTG	7800
GAACCTTGGC	TGGGCGCTAA	CTCCACCCTG	CAGCTTGCCG	TGGGAGACGT	GCAGGGCAAT	7860
GTGTACTTTC	TGAATTGGGA	A				7881

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7886 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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CACTCAGACA	TCCTTTCCTT	GGAGAACCAG	TGTCTGACCA	TGCTCTCTGA	CCTCCAGCCC	180
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TGCCTGACCA	TGCTCCCTGA	CCTCCAGCCT	CTGGAGAAGC	TATGTGGACA	TATGTCTAGT	300
CATCCAGACG	TCCTTTCCTT	GGAAAACCAA	TGTCTAGCTA	CTCTCCCCAC	TGTAAAGAGC	360
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TGTTTCTCTG	AGGAAC TAGA	CCTTCCACCT	GGACCCAGGG	CCCTGAAATC	CATGTCTGCT	540
ACAGCTCAAG	TCCAGGAAGT	AGCCTTGGGT	CAATGGTGTG	TCTCCAAAGA	AAAGGAATTT	600
CAAGAAGAAG	AAAGCACAGA	AGTCCCATGC	CTTTGTACAG	TCTAAGCTTG	GAAGAAGAAG	660
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GTAGTGCCCT	GGCCTCCTTG	GAACCGGAGT	TCATCCTTAA	GGCATCTTTG	TATGCTCGGC	900
AGCAAATTAA	CCTCCGGGAC	ATCGCCAATA	CAGTTCTGGC	TGTGGCTGCC	CTCTTGCCAG	960
CCTGCCGCCC	CCATGTACGA	CGGTATTACT	CCGCCATTGT	TCACCTGCCT	TCAGACTGGA	1020
TCCAGGTAGC	CGAGTTCTAC	CAGAGCCTGG	CAGAAGGGGA	TGAGAAGAAG	TTGGTGTCCC	1080
TGCCTGCCTG	TCTCCGAGCT	GCCATGACCG	ACAAATTTGC	CGAGTTTGAT	GAGTACCAGC	1140
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GTCACCTCCC	TGGGCCGTGG	GAGTCTAGCA	GAGCTGGTCA	GCGGATGAAG	CTCCGAAGGC	1500
CAGAGACCTG	GGAGCGGGAG	CTGAGTTTAC	GGGAAACAA	AGCTTCTGTG	TGGGAGGAGC	1560
TCATAGACAA	TGGGAAACTG	CCCTTCATGG	CCATGCTCCG	GAACCTGTGT	AACCTGCTGC	1620
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CTGTGGTTCA	CAGTCGGCAG	TTTCCATTCA	GATTCCTTAA	TGCTCATGAC	TCTATCGATA	1740
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AACGGATAAT	GATTAGAAAC	TCAAAAAAAA	ATAGGAGGCC	TGCCAGTCGG	AAGCACCTGT	1860
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TTCACTGGAC	CCATGAGTAC	CCTTCAGGGC	GATCCGTGAC	AGAGATGGAG	GTGATGCAAT	3060

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CAGTGCAGCA	GCTGTTGCTG	CCCCATGGGA	GGCTGAGCCT	AGTGACTGGG	CAGGCAGGAC	3540
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TCAACCTCCT	CAGACGCCTC	TGTACCCATC	TGCGTCAAAA	ACTGGGAGAG	CTGAGTGCCC	3720
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CTACCGCACA GGCTCCAGGC CGCGTCAGTC ACCTGATCTG GTACTCGGCA AATTCATTCT 7020
TCGTTCTCAG TGCTAATGAA AACGTCAGCG AGTGGCAAGT GGGACTGAGG AAAGGTTCAA 7080
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CAGGTCTGGG TCTGGCCCCT GATGGCCAGT CTCTCATCTT GATGAAAGAG GATGTGGAAT 7200
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CAGCCCTCCA TGTGCTTCCG GGATTGCTGG TGACAGCTTC GAAGGACAGA GATGTTAAGC 7740
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GAAACTTGTA TTTTCTATCT TGGGAA 7886

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(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2627 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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Lys Leu His Gln His Val Ser Thr His Ser Asp Ile Leu Ser Leu Lys
          35           40           45

Asn Gln Cys Leu Ala Thr Leu Pro Asp Leu Lys Thr Met Glu Lys Pro
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His Gly Tyr Val Ser Ala His Pro Asp Ile Leu Ser Leu Glu Asn Gln
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His	Phe	Ser	Lys	Gly	Leu	Asp	Leu	Ser	Thr	Cys	Pro	Ile	Ala	Leu	Lys	
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Ser	Ile	Ser	Ala	Thr	Glu	Thr	Ala	Gln	Glu	Ala	Thr	Leu	Gly	Arg	Trp	
			180					185					190			
Phe	Asp	Ser	Glu	Glu	Lys	Lys	Gly	Ala	Glu	Thr	Gln	Met	Pro	Ser	Tyr	
		195					200					205				
Ser	Leu	Ser	Leu	Gly	Glu	Glu	Glu	Glu	Val	Glu	Asp	Leu	Ala	Val	Lys	
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Leu	Thr	Ser	Gly	Asp	Ser	Glu	Ser	His	Pro	Glu	Pro	Thr	Asp	His	Val	
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Leu	Gln	Glu	Lys	Lys	Met	Ala	Leu	Leu	Ser	Leu	Leu	Cys	Ser	Thr	Leu	
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Ile	Phe	Glu	Ile	Cys	Arg	Glu	Leu	Ala	Leu	Leu	Glu	Pro	Glu	Phe	Ile	
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305					310					315					320	
His	Leu	Arg	Arg	Tyr	Phe	Cys	Ala	Ile	Val	Gln	Leu	Pro	Ser	Asp	Trp	
				325					330					335		
Ile	Gln	Val	Ala	Glu	Leu	Tyr	Gln	Ser	Leu	Ala	Glu	Gly	Asp	Lys	Asn	
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Lys	Leu	Val	Pro	Leu	Pro	Ala	Cys	Leu	Arg	Thr	Ala	Met	Thr	Asp	Lys	
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Phe	Ala	Gln	Phe	Asp	Glu	Tyr	Gln	Leu	Ala	Lys	Tyr	Asn	Pro	Arg	Lys	
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His	Arg	Ala	Lys	Arg	His	Pro	Arg	Arg	Pro	Pro	Arg	Ser	Pro	Gly	Met	
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Trp	Asp	Ser	Ser	Arg	Ala	Gly	Lys	Arg	Met	Lys	Leu	Ser	Arg	Pro	Glu	
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Thr	Trp	Glu	Arg	Glu	Leu	Ser	Leu	Arg	Gly	Asn	Lys	Ala	Ser	Val	Trp	
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Gln	Phe	Pro	Phe	Arg	Phe	Leu	Asn	Ala	His	Asp	Ala	Ile	Asp	Ala	Leu	
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Gln	Ala	Leu	Glu	Thr	Ala	Val	Asn	Leu	Ser	Val	Lys	His	Ser	Leu	Pro	
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Glu	Glu	Gly	Ile	Leu	Lys	Thr	Ala	Ile	Lys	Leu	Gln	Ala	Gln	Val	Gln	
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Glu	Phe	Asp	Glu	Asn	Asp	Gly	Trp	Ser	Leu	Asn	Thr	Phe	Gly	Lys	Tyr				
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Leu	Gly	Gln	Ser	Met	Asp	Asp	Gly	Met	Ile	Asn	Val	Ala	Lys	Gln	Leu				
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Tyr	Trp	Gln	Arg	Val	Asn	Ser	Lys	Cys	Leu	Phe	Val	Gly	Ile	Leu	Leu				
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Glu	Glu	Asp	Thr	Pro	Ser	Pro	Leu	Ala	Pro	Val	Ser	Gln	Gln	Gly	Trp				
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Glu	Arg	Asp	Leu	Leu	Leu	Arg	Ser	Val	Leu	Pro	Ala	Leu	Gln	Ala	Arg				
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 1490 1495 1500
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Gln Ile Thr Gly Cys Cys Leu Ser Pro Asp Cys Arg Leu Leu Ala Thr
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 Asp Gly Lys Val Gln Val Trp Ser Gly Ser Leu Gly Arg Pro Arg Gly
 1905 1910 1915 1920
 His Leu Gly Ser Leu Ser Leu Ser Pro Ala Leu Ser Val Ala Leu Ser
 1925 1930 1935
 Pro Asp Gly Asp Arg Val Ala Val Gly Tyr Arg Ala Asp Gly Ile Arg
 1940 1945 1950
 Ile Tyr Lys Ile Ser Ser Gly Ser Gln Gly Ala Gln Gly Gln Ala Leu
 1955 1960 1965
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 1970 1975 1980
 Ser Gly Ala Glu Asp Gly Ser Leu Gln Gly Trp Ala Leu Lys Glu Cys
 1985 1990 1995 2000
 Ser Leu Gln Ser Leu Trp Leu Leu Ser Arg Phe Gln Lys Pro Val Leu
 2005 2010 2015
 Gly Leu Ala Thr Ser Gln Glu Leu Leu Ala Ser Ala Ser Glu Asp Phe
 2020 2025 2030
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 2065 2070 2075 2080
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 2085 2090 2095

Val Leu Ile His Ser Phe Pro Ala Cys His Arg Asp Trp Val Thr Gly
 2100 2105 2110
 Cys Ala Trp Thr Lys Asp Asn Leu Leu Ile Ser Cys Ser Ser Asp Gly
 2115 2120 2125
 Ser Val Gly Leu Trp Asp Pro Glu Ser Gly Gln Arg Leu Gly Gln Phe
 2130 2135 2140
 Leu Gly His Gln Ser Ala Val Ser Ala Val Ala Ala Val Glu Glu His
 2145 2150 2155 2160
 Val Val Ser Val Ser Arg Asp Gly Thr Leu Lys Val Trp Asp His Gln
 2165 2170 2175
 Gly Val Glu Leu Thr Ser Ile Pro Ala His Ser Gly Pro Ile Ser His
 2180 2185 2190
 Cys Ala Ala Ala Met Glu Pro Arg Ala Ala Gly Gln Pro Gly Ser Glu
 2195 2200 2205
 Leu Leu Val Val Thr Val Gly Leu Asp Gly Ala Thr Arg Leu Trp His
 2210 2215 2220
 Pro Leu Leu Val Cys Gln Thr His Thr Leu Leu Gly His Ser Gly Pro
 2225 2230 2235 2240
 Val Arg Ala Ala Ala Val Ser Glu Thr Ser Gly Leu Met Leu Thr Ala
 2245 2250 2255
 Ser Glu Asp Gly Ser Val Arg Leu Trp Gln Val Pro Lys Glu Ala Asp
 2260 2265 2270
 Asp Thr Cys Ile Pro Arg Ser Ser Ala Ala Val Thr Ala Val Ala Trp
 2275 2280 2285
 Ala Pro Asp Gly Ser Met Ala Val Ser Gly Asn Gln Ala Gly Glu Leu
 2290 2295 2300
 Ile Leu Trp Gln Glu Ala Lys Ala Val Ala Thr Ala Gln Ala Pro Gly
 2305 2310 2315 2320
 His Ile Gly Ala Leu Ile Trp Ser Ser Ala His Thr Phe Phe Val Leu
 2325 2330 2335
 Ser Ala Asp Glu Lys Ile Ser Glu Trp Gln Val Lys Leu Arg Lys Gly
 2340 2345 2350
 Ser Ala Pro Gly Asn Leu Ser Leu His Leu Asn Arg Ile Leu Gln Glu
 2355 2360 2365
 Asp Leu Gly Val Leu Thr Ser Leu Asp Trp Ala Pro Asp Gly His Phe
 2370 2375 2380
 Leu Ile Leu Ala Lys Ala Asp Leu Lys Leu Leu Cys Met Lys Pro Gly
 2385 2390 2395 2400
 Asp Ala Pro Ser Glu Ile Trp Ser Ser Tyr Thr Glu Asn Pro Met Ile
 2405 2410 2415
 Leu Ser Thr His Lys Glu Tyr Gly Ile Phe Val Leu Gln Pro Lys Asp
 2420 2425 2430

Pro Gly Val Leu Ser Phe Leu Arg Gln Lys Glu Ser Gly Glu Phe Glu
 2435 2440 2445
 Glu Arg Leu Asn Phe Asp Ile Asn Leu Glu Asn Pro Ser Arg Thr Leu
 2450 2455 2460
 Ile Ser Ile Thr Gln Ala Lys Pro Glu Ser Glu Ser Ser Phe Leu Cys
 2465 2470 2475 2480
 Ala Ser Ser Asp Gly Ile Leu Trp Asn Leu Ala Lys Cys Ser Pro Glu
 2485 2490 2495
 Gly Glu Trp Thr Thr Gly Asn Met Trp Gln Lys Lys Ala Asn Thr Pro
 2500 2505 2510
 Glu Thr Gln Thr Pro Gly Thr Asp Pro Ser Thr Cys Arg Glu Ser Asp
 2515 2520 2525
 Ala Ser Met Asp Ser Asp Ala Ser Met Asp Ser Glu Pro Thr Pro His
 2530 2535 2540
 Leu Lys Thr Arg Gln Arg Arg Lys Ile His Ser Gly Ser Val Thr Ala
 2545 2550 2555 2560
 Leu His Val Leu Pro Glu Leu Leu Val Thr Ala Ser Lys Asp Arg Asp
 2565 2570 2575
 Val Lys Leu Trp Glu Arg Pro Ser Met Gln Leu Leu Gly Leu Phe Arg
 2580 2585 2590
 Cys Glu Gly Ser Val Ser Cys Leu Glu Pro Trp Leu Gly Ala Asn Ser
 2595 2600 2605
 Thr Leu Gln Leu Ala Val Gly Asp Val Gln Gly Asn Val Tyr Phe Leu
 2610 2615 2620
 Asn Trp Glu
 2625

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2629 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Glu Lys Leu Cys Gly His Val Pro Gly His Ser Asp Ile Leu Ser
 1 5 10 15
 Leu Lys Asn Arg Cys Leu Thr Met Leu Pro Asp Leu Gln Pro Leu Glu
 20 25 30
 Lys Ile His Gly His Arg Ser Val His Ser Asp Ile Leu Ser Leu Glu
 35 40 45

Asn	Gln	Cys	Leu	Thr	Met	Leu	Ser	Asp	Leu	Gln	Pro	Thr	Glu	Arg	Ile	
50						55					60					
Asp	Gly	His	Ile	Ser	Val	His	Pro	Asp	Ile	Leu	Ser	Leu	Glu	Asn	Arg	
65					70					75					80	
Cys	Leu	Thr	Met	Leu	Pro	Asp	Leu	Gln	Pro	Leu	Glu	Lys	Leu	Cys	Gly	
				85					90					95		
His	Met	Ser	Ser	His	Pro	Asp	Val	Leu	Ser	Leu	Glu	Asn	Gln	Cys	Leu	
			100					105					110			
Ala	Thr	Leu	Pro	Thr	Val	Lys	Ser	Thr	Ala	Leu	Thr	Ser	Pro	Leu	Leu	
		115					120					125				
Gln	Gly	Leu	His	Ile	Ser	His	Thr	Ala	Gln	Ala	Asp	Leu	His	Ser	Leu	
	130					135					140					
Lys	Thr	Ser	Asn	Cys	Leu	Leu	Pro	Glu	Leu	Pro	Thr	Lys	Lys	Thr	Pro	
145					150					155					160	
Cys	Phe	Ser	Glu	Glu	Leu	Asp	Leu	Pro	Pro	Gly	Pro	Arg	Ala	Leu	Lys	
				165					170					175		
Ser	Met	Ser	Ala	Thr	Ala	Gln	Val	Gln	Glu	Val	Ala	Leu	Gly	Gln	Trp	
			180					185					190			
Cys	Val	Ser	Lys	Glu	Lys	Glu	Phe	Gln	Glu	Glu	Glu	Ser	Thr	Glu	Val	
		195					200					205				
Pro	Met	Pro	Leu	Tyr	Ser	Leu	Ser	Leu	Glu	Glu	Glu	Glu	Val	Glu	Ala	
	210					215					220					
Pro	Val	Leu	Lys	Leu	Thr	Ser	Gly	Asp	Ser	Gly	Phe	His	Pro	Glu	Thr	
225					230					235					240	
Thr	Asp	Gln	Val	Leu	Gln	Glu	Lys	Lys	Met	Ala	Leu	Leu	Thr	Leu	Leu	
				245					250					255		
Cys	Ser	Ala	Leu	Ala	Ser	Asn	Val	Asn	Val	Lys	Asp	Ala	Ser	Asp	Leu	
			260					265					270			
Thr	Arg	Ala	Ser	Ile	Leu	Glu	Val	Cys	Ser	Ala	Leu	Ala	Ser	Leu	Glu	
		275					280					285				
Pro	Glu	Phe	Ile	Leu	Lys	Ala	Ser	Leu	Tyr	Ala	Arg	Gln	Gln	Leu	Asn	
	290					295					300					
Leu	Arg	Asp	Ile	Ala	Asn	Thr	Val	Leu	Ala	Val	Ala	Ala	Leu	Leu	Pro	
305					310					315					320	
Ala	Cys	Arg	Pro	His	Val	Arg	Arg	Tyr	Tyr	Ser	Ala	Ile	Val	His	Leu	
				325					330					335		
Pro	Ser	Asp	Trp	Ile	Gln	Val	Ala	Glu	Phe	Tyr	Gln	Ser	Leu	Ala	Glu	
			340					345					350			
Gly	Asp	Glu	Lys	Lys	Leu	Val	Ser	Leu	Pro	Ala	Cys	Leu	Arg	Ala	Ala	
		355					360					365				
Met	Thr	Asp	Lys	Phe	Ala	Glu	Phe	Asp	Glu	Tyr	Gln	Leu	Ala	Lys	Tyr	
						370					380					

Asn 385	Pro	Arg	Lys	His	Arg 390	Ser	Lys	Arg	Arg	Ser 395	Arg	Gln	Pro	Pro	Arg 400
Pro	Gln	Lys	Thr	Glu 405	Arg	Pro	Phe	Ser	Glu 410	Arg	Gly	Lys	Cys	Phe 415	Pro
Lys	Ser	Leu	Trp 420	Pro	Leu	Lys	Asn	Glu 425	Gln	Ile	Thr	Phe	Glu 430	Ala	Ala
Tyr	Asn	Ala 435	Met	Pro	Glu	Lys	Asn 440	Arg	Leu	Pro	Arg	Phe 445	Thr	Leu	Lys
Lys	Leu 450	Val	Glu	Tyr	Leu	His 455	Ile	His	Lys	Pro	Ala 460	Gln	His	Val	Gln
Ala 465	Leu	Leu	Gly	Tyr	Arg 470	Tyr	Pro	Ala	Thr	Leu 475	Glu	Leu	Phe	Ser	Arg 480
Ser	His	Leu	Pro	Gly 485	Pro	Trp	Glu	Ser	Ser 490	Arg	Ala	Gly	Gln	Arg 495	Met
Lys	Leu	Arg	Arg 500	Pro	Glu	Thr	Trp	Glu 505	Arg	Glu	Leu	Ser	Leu 510	Arg	Gly
Asn	Lys	Ala 515	Ser	Val	Trp	Glu	Glu 520	Leu	Ile	Asp	Asn	Gly 525	Lys	Leu	Pro
Phe 530	Met	Ala	Met	Leu	Arg	Asn 535	Leu	Cys	Asn	Leu	Leu 540	Arg	Thr	Gly	Ile
Ser 545	Ala	Arg	His	His	Glu 550	Leu	Val	Leu	Gln	Arg 555	Leu	Gln	His	Glu	Lys 560
Ser	Val	Val	His	Ser 565	Arg	Gln	Phe	Pro	Phe 570	Arg	Phe	Leu	Asn	Ala 575	His
Asp	Ser	Ile	Asp 580	Lys	Leu	Glu	Ala	Gln 585	Leu	Arg	Ser	Lys	Ala 590	Ser	Pro
Phe	Pro	Ser 595	Asn	Thr	Thr	Leu	Met 600	Lys	Arg	Ile	Met	Ile 605	Arg	Asn	Ser
Lys	Lys 610	Asn	Arg	Arg	Pro	Ala 615	Ser	Arg	Lys	His	Leu 620	Cys	Thr	Leu	Thr
Arg 625	Arg	Gln	Leu	Arg	Ala 630	Ala	Met	Thr	Ile	Pro 635	Val	Met	Tyr	Glu	Gln 640
Leu	Lys	Arg	Glu	Lys 645	Leu	Arg	Leu	His	Lys 650	Ala	Arg	Gln	Trp	Asn 655	Cys
Asp	Val	Glu	Leu 660	Leu	Glu	Arg	Tyr	Arg 665	Gln	Ala	Leu	Glu	Thr 670	Ala	Val
Asn	Leu	Ser 675	Val	Lys	His	Asn	Leu 680	Ser	Pro	Met	Pro	Gly 685	Arg	Thr	Leu
Leu 690	Val	Tyr	Leu	Thr	Asp	Ala 695	Asn	Ala	Asp	Arg	Leu 700	Cys	Pro	Lys	Ser
His 705	Ser	Gln	Gly	Pro	Pro 710	Leu	Asn	Tyr	Val	Leu 715	Leu	Leu	Ile	Gly	Met 720

Met	Val	Ala	Arg	Ala	Glu	Gln	Val	Thr	Val	Cys	Leu	Cys	Gly	Gly	Gly	
				725					730					735		
Phe	Val	Lys	Thr	Pro	Val	Leu	Thr	Ala	Asp	Glu	Gly	Ile	Leu	Lys	Thr	
			740					745					750			
Ala	Ile	Lys	Leu	Gln	Ala	Gln	Val	Gln	Glu	Leu	Glu	Gly	Asn	Asp	Glu	
		755					760					765				
Trp	Pro	Leu	Asp	Thr	Phe	Gly	Lys	Tyr	Leu	Leu	Ser	Leu	Ala	Val	Gln	
	770					775					780					
Arg	Thr	Pro	Ile	Asp	Arg	Val	Ile	Leu	Phe	Gly	Gln	Arg	Met	Asp	Thr	
	785				790					795					800	
Glu	Leu	Leu	Lys	Val	Ala	Lys	Gln	Ile	Ile	Trp	Gln	His	Val	Asn	Ser	
				805					810					815		
Lys	Cys	Leu	Phe	Val	Gly	Val	Leu	Leu	Gln	Lys	Thr	Gln	Tyr	Ile	Ser	
			820				825						830			
Pro	Asn	Leu	Asn	Pro	Asn	Asp	Val	Thr	Leu	Ser	Gly	Cys	Thr	Asp	Gly	
		835					840					845				
Ile	Leu	Lys	Phe	Ile	Ala	Glu	His	Gly	Ala	Ser	Arg	Leu	Leu	Glu	His	
	850					855					860					
Val	Gly	Gln	Leu	Asp	Lys	Leu	Phe	Lys	Ile	Pro	Pro	Pro	Pro	Gly	Lys	
	865				870					875					880	
Thr	Gln	Ala	Pro	Ser	Leu	Arg	Pro	Leu	Glu	Glu	Asn	Ile	Pro	Gly	Pro	
				885					890					895		
Leu	Gly	Pro	Ile	Ser	Gln	His	Gly	Trp	Arg	Asn	Ile	Arg	Leu	Phe	Ile	
			900					905					910			
Ser	Ser	Thr	Phe	Arg	Asp	Met	His	Gly	Glu	Arg	Asp	Leu	Leu	Met	Arg	
		915					920					925				
Ser	Val	Leu	Pro	Ala	Leu	Gln	Ala	Arg	Val	Phe	Pro	His	Arg	Ile	Ser	
	930					935					940					
Leu	His	Ala	Ile	Asp	Leu	Arg	Trp	Gly	Ile	Thr	Glu	Glu	Glu	Thr	Arg	
	945				950					955					960	
Arg	Asn	Arg	Gln	Leu	Glu	Val	Cys	Leu	Gly	Glu	Val	Glu	Asn	Ser	Gln	
				965					970					975		
Leu	Phe	Val	Gly	Ile	Leu	Gly	Ser	Arg	Tyr	Gly	Tyr	Ile	Pro	Pro	Ser	
			980					985					990			
Tyr	Asp	Leu	Pro	Asp	His	Pro	His	Phe	His	Trp	Thr	His	Glu	Tyr	Pro	
	995					1000						1005				
Ser	Gly	Arg	Ser	Val	Thr	Glu	Met	Glu	Val	Met	Gln	Phe	Leu	Asn	Arg	
	1010					1015					1020					
Gly	Gln	Arg	Ser	Gln	Pro	Ser	Ala	Gln	Ala	Leu	Ile	Tyr	Phe	Arg	Asp	
	1025				1030					1035					1040	
Pro	Asp	Phe	Leu	Ser	Ser	Val	Pro	Asp	Ala	Trp	Lys	Pro	Asp	Phe	Ile	
				1045					1050					1055		

Ser Glu Ser Glu Glu Ala Ala His Arg Val Ser Glu Leu Lys Arg Tyr
 1060 1065 1070
 Leu His Glu Gln Lys Glu Val Thr Cys Arg Ser Tyr Ser Cys Glu Trp
 1075 1080 1085
 Gly Gly Val Ala Ala Gly Arg Pro Tyr Thr Gly Gly Leu Glu Glu Phe
 1090 1095 1100
 Gly Gln Leu Val Leu Gln Asp Val Trp Ser Met Ile Gln Lys Gln His
 1105 1110 1115 1120
 Leu Gln Pro Gly Ala Gln Leu Glu Gln Pro Thr Ser Ile Ser Glu Asp
 1125 1130 1135
 Asp Leu Ile Gln Thr Ser Phe Gln Gln Leu Lys Thr Pro Thr Ser Pro
 1140 1145 1150
 Ala Arg Pro Arg Leu Leu Gln Asp Thr Val Gln Gln Leu Leu Leu Pro
 1155 1160 1165
 His Gly Arg Leu Ser Leu Val Thr Gly Gln Ala Gly Gln Gly Lys Thr
 1170 1175 1180
 Ala Phe Leu Ala Ser Leu Val Ser Ala Leu Lys Val Pro Asp Gln Pro
 1185 1190 1195 1200
 Asn Glu Pro Pro Phe Val Phe Phe His Phe Ala Ala Ala Arg Pro Asp
 1205 1210 1215
 Gln Cys Leu Ala Leu Asn Leu Leu Arg Arg Leu Cys Thr His Leu Arg
 1220 1225 1230
 Gln Lys Leu Gly Glu Leu Ser Ala Leu Pro Ser Thr Tyr Arg Gly Leu
 1235 1240 1245
 Val Trp Glu Leu Gln Gln Lys Leu Leu Leu Lys Phe Ala Gln Ser Leu
 1250 1255 1260
 Gln Pro Ala Gln Thr Leu Val Leu Ile Ile Asp Gly Ala Asp Lys Leu
 1265 1270 1275 1280
 Val Asp Arg Asn Gly Gln Leu Ile Ser Asp Trp Ile Pro Lys Ser Leu
 1285 1290 1295
 Pro Arg Arg Val His Leu Val Leu Ser Val Ser Ser Asp Ser Gly Leu
 1300 1305 1310
 Gly Glu Thr Leu Gln Gln Ser Gln Gly Ala Tyr Val Val Ala Leu Gly
 1315 1320 1325
 Ser Leu Val Pro Ser Ser Arg Ala Gln Leu Val Arg Glu Glu Leu Ala
 1330 1335 1340
 Leu Tyr Gly Lys Arg Leu Glu Glu Ser Pro Phe Asn Asn Gln Met Arg
 1345 1350 1355 1360
 Leu Leu Leu Ala Lys Gln Gly Ser Ser Leu Pro Leu Tyr Leu His Leu
 1365 1370 1375
 Val Thr Asp Tyr Leu Arg Leu Phe Thr Leu Tyr Glu Gln Val Ser Glu
 1380 1385 1390

Arg Leu Arg Thr Leu Pro Ala Thr Leu Pro Leu Leu Leu Gln His Ile
 1395 1400 1405
 Leu Ser Thr Leu Glu Gln Glu His Gly His Asp Val Leu Pro Gln Ala
 1410 1415 1420
 Leu Thr Ala Leu Glu Val Thr Arg Ser Gly Leu Thr Val Asp Gln Leu
 1425 1430 1435 1440
 His Ala Ile Leu Ser Thr Trp Leu Ile Leu Pro Lys Glu Thr Lys Ser
 1445 1450 1455
 Trp Glu Glu Val Leu Ala Ala Ser His Ser Gly Asn Pro Phe Pro Leu
 1460 1465 1470
 Cys Pro Phe Ala Tyr Leu Val Gln Ser Leu Arg Ser Leu Leu Gly Glu
 1475 1480 1485
 Gly Pro Val Glu Arg Pro Gly Ala Arg Leu Cys Leu Ser Asp Gly Pro
 1490 1495 1500
 Leu Arg Thr Thr Ile Lys Arg Arg Tyr Gly Lys Arg Leu Gly Leu Glu
 1505 1510 1515 1520
 Lys Thr Ala His Val Leu Ile Ala Ala His Leu Trp Lys Thr Cys Asp
 1525 1530 1535
 Pro Asp Ala Ser Gly Thr Phe Arg Ser Cys Pro Pro Glu Ala Leu Lys
 1540 1545 1550
 Asp Leu Pro Tyr His Leu Leu Gln Ser Gly Asn His Gly Leu Leu Ala
 1555 1560 1565
 Glu Phe Leu Thr Asn Leu His Val Val Ala Ala Tyr Leu Glu Val Gly
 1570 1575 1580
 Leu Val Pro Asp Leu Leu Glu Ala His Val Leu Tyr Ala Ser Ser Lys
 1585 1590 1595 1600
 Pro Glu Ala Asn Gln Lys Leu Pro Ala Ala Asp Val Ala Val Phe His
 1605 1610 1615
 Thr Phe Leu Arg Gln Gln Ala Ser Leu Leu Thr Gln Tyr Pro Leu Leu
 1620 1625 1630
 Leu Leu Gln Gln Ala Ala Ser Gln Pro Glu Glu Ser Pro Val Cys Cys
 1635 1640 1645
 Gln Ala Pro Leu Leu Thr Gln Arg Trp His Asp Gln Phe Thr Leu Lys
 1650 1655 1660
 Trp Ile Asn Lys Pro Gln Thr Leu Lys Gly Gln Gln Ser Leu Ser Leu
 1665 1670 1675 1680
 Thr Met Ser Ser Ser Pro Thr Ala Val Ala Phe Ser Pro Asn Gly Gln
 1685 1690 1695
 Arg Ala Ala Val Gly Thr Ala Ser Gly Thr Ile Tyr Leu Leu Asn Leu
 1700 1705 1710
 Lys Thr Trp Gln Glu Glu Lys Ala Val Val Ser Gly Cys Asp Gly Ile
 1715 1720 1725

Ser Ser Phe Ala Phe Leu Ser Asp Thr Ala Leu Phe Leu Thr Thr Phe
 1730 1735 1740
 Asp Gly His Leu Glu Leu Trp Asp Leu Gln His Gly Cys Trp Val Phe
 1745 1750 1755 1760
 Gln Thr Lys Ala His Gln Tyr Gln Ile Thr Gly Cys Cys Leu Ser Pro
 1765 1770 1775
 Asp Arg Arg Leu Leu Ala Thr Val Cys Leu Gly Gly Tyr Leu Lys Leu
 1780 1785 1790
 Trp Asp Thr Val Arg Gly Gln Leu Ala Phe Gln Tyr Thr His Pro Lys
 1795 1800 1805
 Ser Leu Asn Cys Val Ala Phe His Pro Glu Gly Gln Val Val Ala Thr
 1810 1815 1820
 Gly Ser Trp Ala Gly Ser Ile Thr Phe Phe Gln Ala Asp Gly Leu Lys
 1825 1830 1835 1840
 Val Thr Lys Glu Leu Gly Ala Pro Gly Pro Ser Val Cys Ser Leu Ala
 1845 1850 1855
 Phe Asn Lys Pro Gly Lys Ile Val Ala Val Gly Arg Ile Asp Gly Thr
 1860 1865 1870
 Val Glu Leu Trp Ala Trp Gln Glu Gly Ala Arg Leu Ala Ala Phe Pro
 1875 1880 1885
 Ala Gln Cys Gly Cys Val Ser Ala Val Leu Phe Leu His Ala Gly Asp
 1890 1895 1900
 Arg Phe Leu Thr Ala Gly Glu Asp Gly Lys Ala Gln Leu Trp Ser Gly
 1905 1910 1915 1920
 Phe Leu Gly Arg Pro Arg Gly Cys Leu Gly Ser Leu Pro Leu Ser Pro
 1925 1930 1935
 Ala Leu Ser Val Ala Leu Asn Pro Asp Gly Asp Gln Val Ala Val Gly
 1940 1945 1950
 Tyr Arg Glu Asp Gly Ile Asn Ile Tyr Lys Ile Ser Ser Gly Ser Gln
 1955 1960 1965
 Gly Pro Gln His Gln Glu Leu Asn Val Ala Val Ser Ala Leu Val Trp
 1970 1975 1980
 Leu Ser Pro Ser Val Leu Val Ser Gly Ala Glu Asp Gly Ser Leu His
 1985 1990 1995 2000
 Gly Trp Met Phe Lys Gly Asp Ser Leu His Ser Leu Trp Leu Leu Ser
 2005 2010 2015
 Arg Tyr Gln Lys Pro Val Leu Gly Leu Ala Ala Ser Arg Glu Leu Met
 2020 2025 2030
 Ala Ala Ala Ser Glu Asp Phe Thr Val Arg Leu Trp Pro Arg Gln Leu
 2035 2040 2045
 Leu Thr Gln Pro His Val His Ala Val Glu Leu Pro Cys Cys Ala Glu
 2050 2055 2060

Leu Arg Gly His Glu Gly Pro Val Cys Cys Cys Ser Phe Ser Pro Asp
 2065 2070 2075 2080
 Gly Gly Ile Leu Ala Thr Ala Gly Arg Asp Arg Asn Leu Leu Cys Trp
 2085 2090 2095
 Asp Met Lys Ile Ala Gln Ala Pro Leu Leu Ile His Thr Phe Ser Ser
 2100 2105 2110
 Cys His Arg Asp Trp Ile Thr Gly Cys Ala Trp Thr Lys Asp Asn Ile
 2115 2120 2125
 Leu Val Ser Cys Ser Ser Asp Gly Ser Val Gly Leu Trp Asn Pro Glu
 2130 2135 2140
 Ala Gly Gln Gln Leu Gly Gln Phe Ser Gly His Gln Ser Ala Val Ser
 2145 2150 2155 2160
 Ala Val Val Ala Val Glu Glu His Ile Val Ser Val Ser Arg Asp Gly
 2165 2170 2175
 Thr Leu Lys Val Trp Asp His Gln Gly Val Glu Leu Thr Ser Ile Pro
 2180 2185 2190
 Ala His Ser Gly Pro Ile Ser Gln Cys Ala Ala Ala Leu Glu Pro Arg
 2195 2200 2205
 Pro Gly Gly Gln Pro Gly Ser Glu Leu Leu Val Val Thr Val Gly Leu
 2210 2215 2220
 Asp Gly Ala Thr Lys Leu Trp His Pro Leu Leu Val Cys Gln Ile Arg
 2225 2230 2235 2240
 Thr Leu Gln Gly His Ser Gly Pro Val Thr Ala Ala Ala Ala Ser Glu
 2245 2250 2255
 Ala Ser Gly Leu Leu Leu Thr Ser Asp Asp Ser Ser Val Gln Leu Trp
 2260 2265 2270
 Gln Ile Pro Lys Glu Ala Asp Asp Ser Tyr Lys Pro Arg Ser Ser Val
 2275 2280 2285
 Ala Ile Thr Ala Val Ala Trp Ala Pro Asp Gly Ser Met Val Val Ser
 2290 2295 2300
 Gly Asn Glu Ala Gly Glu Leu Thr Leu Trp Gln Gln Ala Lys Ala Val
 2305 2310 2315 2320
 Ala Thr Ala Gln Ala Pro Gly Arg Val Ser His Leu Ile Trp Tyr Ser
 2325 2330 2335
 Ala Asn Ser Phe Phe Val Leu Ser Ala Asn Glu Asn Val Ser Glu Trp
 2340 2345 2350
 Gln Val Gly Leu Arg Lys Gly Ser Thr Ser Thr Ser Ser Ser Leu His
 2355 2360 2365
 Leu Lys Arg Val Leu Gln Glu Asp Trp Gly Val Leu Thr Gly Leu Gly
 2370 2375 2380
 Leu Ala Pro Asp Gly Gln Ser Leu Ile Leu Met Lys Glu Asp Val Glu
 2385 2390 2395 2400

Leu Leu Glu Met Lys Pro Gly Ser Ile Pro Ser Ser Ile Cys Arg Arg
 2405 2410 2415
 Tyr Gly Val His Ser Ser Ile Leu Cys Thr Ser Lys Glu Tyr Gly Leu
 2420 2425 2430
 Phe Tyr Leu Gln Gln Gly Asp Ser Gly Leu Leu Ser Ile Leu Glu Gln
 2435 2440 2445
 Lys Glu Ser Gly Glu Phe Glu Glu Ile Leu Asp Phe Asn Leu Asn Leu
 2450 2455 2460
 Asn Asn Pro Asn Gly Ser Pro Val Ser Ile Thr Gln Ala Lys Pro Glu
 2465 2470 2475 2480
 Ser Glu Ser Ser Leu Leu Cys Ala Thr Ser Asp Gly Met Leu Trp Asn
 2485 2490 2495
 Leu Ser Glu Cys Thr Ser Glu Gly Glu Trp Ile Val Asp Asn Ile Trp
 2500 2505 2510
 Gln Lys Lys Ala Lys Lys Pro Lys Thr Gln Thr Leu Glu Thr Glu Leu
 2515 2520 2525
 Ser Pro His Ser Glu Leu Asp Phe Ser Ile Asp Cys Trp Ile Asp Pro
 2530 2535 2540
 Thr Asn Leu Lys Ala Gln Gln Cys Lys Lys Ile His Leu Gly Ser Val
 2545 2550 2555 2560
 Thr Ala Leu His Val Leu Pro Gly Leu Leu Val Thr Ala Ser Lys Asp
 2565 2570 2575
 Arg Asp Val Lys Leu Trp Glu Arg Pro Ser Met Gln Leu Leu Gly Leu
 2580 2585 2590
 Phe Arg Cys Glu Gly Pro Val Ser Cys Leu Glu Pro Trp Met Glu Pro
 2595 2600 2605
 Ser Ser Pro Leu Gln Leu Ala Val Gly Asp Thr Gln Gly Asn Leu Tyr
 2610 2615 2620
 Phe Leu Ser Trp Glu
 2625

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
- (A) DESCRIPTION: /desc = "Oligo nucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCTCTGCGGC CGCTACANNN NNNNNT

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligo nucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGAGACGCCG GCGA

14

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligo nucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TCGACCCACG CGTCCG

16

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligo nucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGGTGCGCAG GC

12

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligo nucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGTAACACGA CGGCCAGT

18

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligo nucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAGGAAACAG CTATGACC

18

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligo nucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CAATTAACCC TCACTAAAG

19

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 154 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligo nucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGTACCGCCA GCCGAGCCAC ATCGCTCAGA CACCATGATC GCAAATGTGA ATATTGCTCA 60

GGAACAAAAG CTTATTTCTG AAGAAGACTT GGCTCAGGAA CAAAAGCTTA TTTCTGAAGA 120

AGACTTGGCT CAGCAGAGTG GCGGAGGACT CGAG 154

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2848 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CACGCGTCCG	GGCAGCGCTG	CGTCCGTGCTG	CGCACGTGGG	AAGCCCTGGC	CCCGGCCACC	60
CCCGCGATGC	CGCGCGCTCC	CCGCTGCCGA	GCCGTGCGCT	CCCTGCTGCG	CAGCCACTAC	120
CGCGAGGTGC	TGCCGCTGGC	CACGTTTCGTG	CGGCGCCTGG	GGCCCCAGGG	CTGGCGGCTG	180
GTGCAGCGCG	GGGACCCGGC	GGCTTTCCGC	GCGCTGGTGG	CCCAGTGCCT	GGTGTGCGTG	240
CCCTGGGACG	CACGGCCGCC	CCCCGCCGCC	CCCTCCTTCC	GCCAGGTGTC	CTGCCTGAAG	300
GAGCTGGTGG	CCCGAGTGCT	GCAGAGGCTG	TGCGAGCGCG	GCGCGAAGAA	CGTGCTGGCC	360
TTCGGCTTCG	CGCTGCTGGA	CGGGGCCCCG	GGGGGCCCCC	CCGAGGCCTT	CACCACCAGC	420
GTGCGCAGCT	ACCTGCCCAA	CACGGTGACC	GACGCACTGC	GGGGGAGCGG	GGCGTGGGGG	480
CTGCTGCTGC	GCCGCGTGGG	CGACGACGTG	CTGGTTCACC	TGCTGGCACG	CTGCGCGCTC	540
TTTGTGCTGG	TGGCTCCCAG	CTGCGCCTAC	CAGGTGTGCG	GGCCGCCGCT	GTACCAGCTC	600
GGCGCTGCCA	CTCAGGCCCG	GCCCCGCCA	CACGCTAGTG	GACCCCGAAG	GCGTCTGGGA	660
TGCGAACGGG	CCTGGAACCA	TAGCGTCAGG	GAGGCCGGGG	TCCCCCTGGG	CCTGCCAGCC	720
CCGGGTGCGA	GGAGGCGCGG	GGGAGTGCC	AGCCGAAGTC	TGCCGTTGCC	CAAGAGGCCC	780
AGGCGTGCGG	CTGCCCCCTGA	GCCGGAGCGG	ACGCCCCGTTG	GGCAGGGGTC	CTGGGCCCCAC	840
CCGGGCAGGA	CGCGTGGAAC	GAGTGACCGT	GGTTTCTGTG	TGGTGTCAAC	TGCCAGACCC	900
GCCGAAGAAG	CCACCTCTTT	GGAGGGTGCG	CTCTCTGGCA	CGCGCCACTC	CCACCCATCC	960
GTGGGCCCGC	AGCACCACGC	GGGCCCCCCA	TCCACATCGC	GGCCACCACG	TCCCTGGGAC	1020
ACGCCTTGTC	CCCCGGTGTA	CGCCGAGACC	AAGCACTTCC	TCTACTCCTC	AGGCGACAAG	1080
GAGCAGCTGC	GGCCCTCCTT	CCTACTCAGC	TCTCTGAGGC	CCAGCCTGAC	TGGCGCTCGG	1140
AGGCTCGTGG	AGACCATCTT	TCTGGGTTCC	AGGCCCTGGA	TGCCAGGGAC	TCCCCGCAGG	1200
TTGCCCCGCC	TGCCCCAGCG	CTACTGGCAA	ATGCGGCCCC	TGTTTCTGGA	GCTGCTTGGG	1260
AACCACGCGC	AGTGCCCCCTA	CGGGGTGCTC	CTCAAGACGC	ACTGCCCCGCT	GCGAGCTGCG	1320
GTCACCCCAG	CAGCCGGTGT	CTGTGCCCCG	GAGAAGCCCC	AGGGCTCTGT	GGCGGCCCCC	1380
GAGGAGGAGG	ACACAGACCC	CCGTCGCCTG	GTGCAGCTGC	TCCGCCAGCA	CAGCAGCCCC	1440
TGGCAGGTGT	ACGGCTTCGT	GCGGGCCTGC	CTGCGCCGGC	TGGTGCCCCC	AGGCCTCTGG	1500
GGCTCCAGGC	ACAACGAACG	CCGCTTCCTC	AGGAACACCA	AGAAGTTCAT	CTCCCTGGGG	1560
AAGCATGCCA	AGCTCTCGCT	GCAGGAGCTG	ACGTGGAAGA	TGAGCGTGCG	GGACTGCGCT	1620
TGGCTGCGCA	GGAGCCCAGG	GGTTGGCTGT	GTTCCGGCCG	CAGAGCACCG	TCTGCGTGAG	1680
GAGATCCTGG	CCAAGTTCCT	GCACTGGCTG	ATGAGTGTGT	ACGTCGTCGA	GCTGCTCAGG	1740
TCTTTCTTTT	ATGTCACGGA	GACCACGTTT	CAAAAGAACA	GGCTCTTTTT	CTACCGGAAG	1800

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AGTGTCTGGA GCAAGTTGCA AAGCATTGGA ATCAGACAGC ACTTGAAGAG GGTGCAGCTG      1860
CGGGAGCTGT CGGAAGCAGA GGTCAGGCAG CATCGGGAAG CCAGGCCCGC CCTGCTGACG      1920
TCCAGACTCC GCTTCATCCC CAAGCCTGAC GGGCTGCGGC CGATTGTGAA CATGGACTAC      1980
GTCGTGGGAG CCAGAACGTT CCGCAGAGAA AAGAGGGCCG AGCGTCTCAC CTCGAGGGTG      2040
AAGGCACTGT TCAGCGTGCT CAACTACGAG CGGGCGCGGC GCGCCGGCCT CCTGGGCGCC      2100
TCTGTGCTGG GCCTGGACGA TATCCACAGG GCCTGGCGCA CCTTCGTGCT GCGTGTGCGG      2160
GCCCAGGACC CGCCGCCTGA GCTGTACTTT GTCAAGGTGG ATGTGACGGG CGCGTACGAC      2220
ACCATCCCCC AGGACAGGCT CACGGAGGTC ATCGCCAGCA TCATCAAACC CCAGAACACG      2280
TACTGCGTGC GTCGGTATGC CGTGGTCCAG AAGGCCGCCC ATGGGCACGT CCGCAAGGCC      2340
TTCAAGAGCC ACGTCTCTAC CTTGACAGAC CTCCAGCCGT ACATGCGACA GTTCGTGGCT      2400
CACCTGCAGG AGACCAGCCC GCTGAGGGAT GCCGTCTGTA TCGAGCAGAG CTCCTCCCTG      2460
AATGAGGCCA GCAGTGGCCT CTTGACGTC TTCTACGCT TCATGTGCCA CCACGCCGTG      2520
CGCATCAGGG GCAAGTCCTA CGTCCAGTGC CAGGGGATCC CGCAGGGCTC CATCCTCTCC      2580
ACGCTGCTCT GCAGCCTGTG CTACGGCGAC ATGGAGAACA AGCTGTTTGC GGGGATTCGG      2640
CGGGACGGGC TGCTCCTGCG TTTGGTGGAT GATTTCCTGT TGGTGACACC TCACCTCACC      2700
CACGCGAAAA CCTTCCTCAG GACCCTGGTC CGAGGTGTCC CTGAGTATGG CTGCGTGGTG      2760
AACTTGCGGA AGACAGTGGT GAACTTCCCT GTAGAAGACG AGGCCCTGGG TGGCACGGCT      2820
TTTGTTTCAGA TGCCGGCCCA CGGCCTAT                                     2848

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(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 949 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```

His Ala Ser Gly Gln Arg Cys Val Leu Leu Arg Thr Trp Glu Ala Leu
1           5           10           15
Ala Pro Ala Thr Pro Ala Met Pro Arg Ala Pro Arg Cys Arg Ala Val
20           25           30
Arg Ser Leu Leu Arg Ser His Tyr Arg Glu Val Leu Pro Leu Ala Thr
35           40           45
Phe Val Arg Arg Leu Gly Pro Gln Gly Trp Arg Leu Val Gln Arg Gly
50           55           60
Asp Pro Ala Ala Phe Arg Ala Leu Val Ala Gln Cys Leu Val Cys Val
65           70           75           80

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Pro	Trp	Asp	Ala	Arg	Pro	Pro	Pro	Ala	Ala	Pro	Ser	Phe	Arg	Gln	Val	
				85					90					95		
Ser	Cys	Leu	Lys	Glu	Leu	Val	Ala	Arg	Val	Leu	Gln	Arg	Leu	Cys	Glu	
			100					105					110			
Arg	Gly	Ala	Lys	Asn	Val	Leu	Ala	Phe	Gly	Phe	Ala	Leu	Leu	Asp	Gly	
		115					120					125				
Ala	Arg	Gly	Gly	Pro	Pro	Glu	Ala	Phe	Thr	Thr	Ser	Val	Arg	Ser	Tyr	
	130					135					140					
Leu	Pro	Asn	Thr	Val	Thr	Asp	Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp	Gly	
145					150					155					160	
Leu	Leu	Leu	Arg	Arg	Val	Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	
				165					170					175		
Arg	Cys	Ala	Leu	Phe	Val	Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	
			180					185					190			
Cys	Gly	Pro	Pro	Leu	Tyr	Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	
		195					200					205				
Pro	Pro	His	Ala	Ser	Gly	Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	
	210					215					220					
Trp	Asn	His	Ser	Val	Arg	Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	
225					230					235					240	
Pro	Gly	Ala	Arg	Arg	Arg	Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	
				245					250					255		
Pro	Lys	Arg	Pro	Arg	Arg	Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	
			260					265					270			
Val	Gly	Gln	Gly	Ser	Trp	Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	
		275					280					285				
Asp	Arg	Gly	Phe	Cys	Val	Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	
	290					295					300					
Thr	Ser	Leu	Glu	Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	
305					310					315					320	
Val	Gly	Arg	Gln	His	His	Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	
				325					330					335		
Arg	Pro	Trp	Asp	Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	
			340					345					350			
Phe	Leu	Tyr	Ser	Ser	Gly	Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	
		355					360					365				
Leu	Ser	Ser	Leu	Arg	Pro	Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	
	370					375					380					
Thr	Ile	Phe	Leu	Gly	Ser	Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	
385					390					395					400	
Leu	Pro	Arg	Leu	Pro	Gln	Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	
				405					410					415		

Glu	Leu	Leu	Gly	Asn	His	Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	420	425					430
Thr	His	Cys	Pro	Leu	Arg	Ala	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys		440					445
Ala	Arg	Glu	Lys	Pro	Gln	Gly	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	450	455					460
Thr	Asp	Pro	Arg	Arg	Leu	Val	Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	465	470					480
Trp	Gln	Val	Tyr	Gly	Phe	Val	Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro		485					490
Pro	Gly	Leu	Trp	Gly	Ser	Arg	His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn		500					510
Thr	Lys	Lys	Phe	Ile	Ser	Leu	Gly	Lys	His	Ala	Lys	Leu	Ser	Leu	Gln		515					520
Glu	Leu	Thr	Trp	Lys	Met	Ser	Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg		530					535
Ser	Pro	Gly	Val	Gly	Cys	Val	Pro	Ala	Ala	Glu	His	Arg	Leu	Arg	Glu	545	550					555
Glu	Ile	Leu	Ala	Lys	Phe	Leu	His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val		565					570
Glu	Leu	Leu	Arg	Ser	Phe	Phe	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys		580					585
Asn	Arg	Leu	Phe	Phe	Tyr	Arg	Lys	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser		595					600
Ile	Gly	Ile	Arg	Gln	His	Leu	Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser		610					615
Glu	Ala	Glu	Val	Arg	Gln	His	Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu	Thr	625	630					635
Ser	Arg	Leu	Arg	Phe	Ile	Pro	Lys	Pro	Asp	Gly	Leu	Arg	Pro	Ile	Val		645					650
Asn	Met	Asp	Tyr	Val	Val	Gly	Ala	Arg	Thr	Phe	Arg	Arg	Glu	Lys	Arg		660					665
Ala	Glu	Arg	Leu	Thr	Ser	Arg	Val	Lys	Ala	Leu	Phe	Ser	Val	Leu	Asn		675					680
Tyr	Glu	Arg	Ala	Arg	Arg	Pro	Gly	Leu	Leu	Gly	Ala	Ser	Val	Leu	Gly		690					695
Leu	Asp	Asp	Ile	His	Arg	Ala	Trp	Arg	Thr	Phe	Val	Leu	Arg	Val	Arg	705	710					715
Ala	Gln	Asp	Pro	Pro	Pro	Glu	Leu	Tyr	Phe	Val	Lys	Val	Asp	Val	Thr		725					730
Gly	Ala	Tyr	Asp	Thr	Ile	Pro	Gln	Asp	Arg	Leu	Thr	Glu	Val	Ile	Ala		740					745

Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val
 755 760 765
 Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His
 770 775 780
 Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala
 785 790 795 800
 His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln
 805 810 815
 Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu
 820 825 830
 Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val
 835 840 845
 Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys
 850 855 860
 Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg
 865 870 875 880
 Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr
 885 890 895
 Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly
 900 905 910
 Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn
 915 920 925
 Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met
 930 935 940
 Pro Ala His Gly Leu
 945

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
- (A) DESCRIPTION: /desc = "Oligo nucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCAAGTTCCT GCACTGGCTG AT

22

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligo nucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCTCGTAGTT GAGCAGCTG AA

22

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Phe Phe Tyr Val Thr Glu
 1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 949 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TCCCCTGGTG CGGCCTGCTG CTGGATACCC GGACCCTGGA GGTGCAGAGC GACTACTCCA	60
GCTATGCCCCG GACCTCCATC AGAGCCAGTC TCACCTTCAA CCGCGGCTTC AAGGCTGGGA	120
GGAACATGCG TCGCAAATC TTTGGGGTCT TCGCGCTGAA GTGTACAGC CTGTTTCTGG	180
ATTTGCAGGT GAACAGCCTC CAGACGGTGT GCACCAACAT CTACAAGATC CTCCTGCTGC	240
AGGCGTACAG GTTTCACGCA TGTGTGCTGC AGCTCCCATT TCATCAGCAA GTTTGGAAGA	300
ACCCACATT TTTCTGCGC GTCATCTCTG ACACGGCCTC CCTCTGCTAC TCCATCCTGA	360
AAGCCAAGAA CGCAGGGATG TCGCTGGGGG CCAAGGGCGC CGCCGGCCCT CTGCCCTCCG	420
AGGCCGTGCA GTGGCTGTGC CACCAAGCAT TCCTGCTCAA GCTGACTCGA CACCGTGTCA	480
CCTACGTGCC ACTCCTGGGG TCACTCAGGA CAGCCCAGAC GCAGCTGAGT CGGAAGCTCC	540
CGGGGACGAC GCTGACTGCC CTGGAGGCCG CAGCCAACCC GGCAC'TGCCC TCAGACTTCA	600
AGACCATCCT GGACTGATGG CCACCCGCCC ACAGCCAGGC CGAGAGCAGA CACCAGCAGC	660
CCTGTACGCG CGGGCTCTAC GTCCCAGGGA GGGAGGGGCG GCCCACACCC AGGCCCGCAC	720
CGCTGGGAGT CTGAGGCCTG AGTGAGTGTT TGGCCGAGGC CTGCATGTCC GGCTGAAGGC	780

TGAGTGTCCG	GCTGAGGCCT	GAGCGAGTGT	CCAGCCAAGG	GCTGAGTGTC	CAGCACACCT	840
GCCGTCTTCA	CTTCCCCACA	GGCTGGCGCT	CGGCTCCACC	CCAGGGCCAG	CTTTTCTCTCA	900
CCAGGAGCCC	GGCTTCCACT	CCCCACATAG	GAATAGTCCA	TCCCCTGAT		949

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3798 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCACGCGTCC	GGGCAGCGCT	GCGTCCTGCT	GCGCACGTGG	GAAGCCCTGG	CCCCGGCCAC	60
CCCCGCGATG	CCGCGCGCTC	CCCGCTGCCG	AGCCGTGCGC	TCCCTGCTGC	GCAGCCACTA	120
CCGCGAGGTG	CTGCCGCTGG	CCACGTTCTG	GCGGCGCCTG	GGGCCCCAGG	GCTGGCGGCT	180
GGTGCAGCGC	GGGGACCCGG	CGGCTTTCCG	CGCGCTGGTG	GCCCAGTGCC	TGGTGTGCGT	240
GCCCTGGGAC	GCACGGCCGC	CCCCCGCCGC	CCCCTCCTTC	CGCCAGGTGT	CCTGCCTGAA	300
GGAGCTGGTG	GCCCCAGTGC	TGCAGAGGCT	GTGCGAGCGC	GGCGCGAAGA	ACGTGCTGGC	360
CTTCGGCTTC	GCGCTGCTGG	ACGGGGCCCCG	CGGGGGCCCC	CCCGAGGCCT	TCACCACCAG	420
CGTGCGCAGC	TACCTGCCCA	ACACGGTGAC	CGACGCACTG	CGGGGGAGCG	GGGCGTGGGG	480
GCTGCTGCTG	CGCCGCGTGG	GCGACGACGT	GCTGGTTTCA	CTGCTGGCAC	GCTGCGCGCT	540
CTTTGTGCTG	GTGGCTCCCA	GCTGCGCCTA	CCAGGTGTGC	GGGCCGCCGC	TGTACCAGCT	600
CGGCGCTGCC	ACTCAGGCCC	GGCCCCCGCC	ACACGCTAGT	GGACCCCGAA	GGCGTCTGGG	660
ATGCGAACGG	GCCTGGAACC	ATAGCGTCAG	GGAGGCCGGG	GTCCCCCTGG	GCCTGCCAGC	720
CCCGGGTGCG	AGGAGGCGCG	GGGGCAGTGC	CAGCCGAAGT	CTGCCGTTGC	CCAAGAGGCC	780
CAGGCGTGGC	GCTGCCCCCTG	AGCCGGAGCG	GACGCCCGTT	GGGCAGGGGT	CCTGGGCCCA	840
CCCGGGCAGG	ACGCGTGGAC	CGAGTGACCG	TGGTTTCTGT	GTGGTGTTCAC	CTGCCAGACC	900
CGCCGAAGAA	GCCACCTCTT	TGGAGGGTGC	GCTCTCTGGC	ACGCGCCACT	CCCACCCATC	960
CGTGGGCCGC	CAGCACCACG	CGGGCCCCCC	ATCCACATCG	CGGCCACCAC	GTCCCTGGGA	1020
CACGCCTTGT	CCCCCGGTGT	ACGCCGAGAC	CAAGCACTTC	CTCTACTCCT	CAGGCGACAA	1080
GGAGCAGCTG	CGGCCCTCCT	TCCTACTCAG	CTCTCTGAGG	CCCAGCCTGA	CTGGCGCTCG	1140
GAGGCTCGTG	GAGACCATCT	TTCTGGGTTC	CAGGCCCTGG	ATGCCAGGGA	CTCCCCGCAG	1200
GTTGCCCCGC	CTGCCCCAGC	GCTACTGGCA	AATGCGGCCC	CTGTTTCTGG	AGCTGCTTGG	1260
GAACCACGCG	CAGTGCCCCCT	ACGGGGTGCT	CCTCAAGACG	CACTGCCCCG	TGCGAGCTGC	1320

GGTCACCCCA	GCAGCCGGTG	TCTGTGCCCCG	GGAGAAGCCC	CAGGGCTCTG	TGGCGGCCCC	1380
CGAGGAGGAG	GACACAGACC	CCCGTCGCCT	GGTGCAGCTG	CTCCGCCAGC	ACAGCAGCCC	1440
CTGGCAGGTG	TACGGCTTCG	TGCGGGCCTG	CCTGCGCCGG	CTGGTGCCCC	CAGGCCTCTG	1500
GGGCTCCAGG	CACAACGAAC	GCCGCTTCCT	CAGGAACACC	AAGAAGTTCA	TCTCCCTGGG	1560
GAAGCATGCC	AAGCTCTCGC	TGCAGGAGCT	GACGTGGAAG	ATGAGCGTGC	GGGACTGCGC	1620
TTGGCTGCGC	AGGAGCCCAG	GGGTTGGCTG	TGTTCCGGCC	GCAGAGCACC	GTCTGCGTGA	1680
GGAGATCCTG	GCCAAGTTCC	TGCACTGGCT	GATGAGTGTG	TACGTCGTCG	AGCTGCTCAG	1740
GTCTTTCTTT	TATGTCACGG	AGACCACGTT	TCAAAAGAAC	AGGCTCTTTT	TCTACCGGAA	1800
GAGTGTCTGG	AGCAAGTTGC	AAAGCATTGG	AATCAGACAG	CAC TTGAAGA	GGGTGCAGCT	1860
GCGGGAGCTG	TCGGAAGCAG	AGGTCAGGCA	GCATCGGGAA	GCCAGGCCCG	CCCTGCTGAC	1920
GTCCAGACTC	CGCTTCATCC	CCAAGCCTGA	CGGGCTGCGG	CCGATTGTGA	ACATGGACTA	1980
CGTCGTGGGA	GCCAGAACGT	TCCGCAGAGA	AAAGAGGGCC	GAGCGTCTCA	CCTCGAGGGT	2040
GAAGGCACTG	TTCAAGCGTG	TCAACTACGA	GCGGGCGCGG	CGCCCCGGCC	TCCTGGGCGC	2100
CTCTGTGCTG	GGCCTGGACG	ATATCCACAG	GGCCTGGCGC	ACCTTCGTGC	TGCGTGTGCG	2160
GGCCCAGGAC	CCGCCGCCTG	AGCTGTACTT	TGTCAAGGTG	GATGTGACGG	GCGCGTACGA	2220
CACCATCCCC	CAGGACAGGC	TCACGGAGGT	CATCGCCAGC	ATCATCAAAC	CCCAGAACAC	2280
GTACTGCGTG	CGTCGGTATG	CCGTGGTCCA	GAAGGCCGCC	CATGGGCACG	TCCGCAAGGC	2340
CTTCAAGAGC	CACGTCTCTA	CCTTGACAGA	CCTCCAGCCG	TACATGCGAC	AGTTTCGTGGC	2400
TCACCTGCAG	GAGACCAGCC	CGCTGAGGGA	TGCCGTCGTC	ATCGAGCAGA	GCTCCTCCCT	2460
GAATGAGGCC	AGCAGTGGCC	TCTTCGACGT	CTTCCTACGC	TTTCATGTGCC	ACCACGCCGT	2520
GCGCATCAGG	GGCAAGTCCT	ACGTCCAGTG	CCAGGGGATC	CCGCAGGGCT	CCATCCTCTC	2580
CACGCTGCTC	TGCAGCCTGT	GCTACGGCGA	CATGGAGAAC	AAGCTGTTTG	CGGGGATTCTG	2640
GCGGGACGGG	CTGCTCCTGC	GTTTGGTGGA	TGATTTCTTG	TTGGTGACAC	CTCACCTCAC	2700
CCACGCGAAA	ACCTTCCTCA	GGACCCTGGT	CCGAGGTGTC	CCTGAGTATG	GCTGCGTGGT	2760
GAAC TTGCGG	AAGACAGTGG	TGAACTTCCC	TGTAGAAGAC	GAGGCCCTGG	GTGGCACGGC	2820
TTTTGTTCAG	ATGCCGGCCC	ACGGCCTATT	CCCCTGGTGC	GGCCTGCTGC	TGGATACCCG	2880
GACCCTGGAG	GTGCAGAGCG	ACTACTCCAG	CTATGCCCGG	ACCTCCATCA	GAGCCAGTCT	2940
CACCTTCAAC	CGCGGCTTCA	AGGCTGGGAG	GAACATGCGT	CGCAAAC TCT	TTGGGGTCTT	3000
GCGGCTGAAG	TGTCACAGCC	TGTTTCTGGA	TTTGCAGGTG	AACAGCCTCC	AGACGGTGTG	3060
CACCAACATC	TACAAGATCC	TCCTGCTGCA	GGCGTACAGG	TTTCACGCAT	GTGTGCTGCA	3120
GCTCCCATTT	CATCAGCAAG	TTTGGAAGAA	CCCCACATTT	TTCTGCGCG	TCATCTCTGA	3180

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CACGGCCTCC CTCTGCTACT CCATCCTGAA AGCCAAGAAC GCAGGGATGT CGCTGGGGGC      3240
CAAGGGCGCC GCCGGCCCTC TGCCCTCCGA GGCCGTGCAG TGGCTGTGCC ACCAAGCATT      3300
CCTGCTCAAG CTGACTCGAC ACCGTGTCAC CTACGTGCCA CTCCTGGGGT CACTCAGGAC      3360
AGCCCAGACG CAGCTGAGTC GGAAGCTCCC GGGGACGACG CTGACTGCCC TGGAGGCCGC      3420
AGCCAACCCG GCACTGCCCT CAGACTTCAA GACCATCCTG GACTGATGGC CACCCGCCCA      3480
CAGCCAGGCC GAGAGCAGAC ACCAGCAGCC CTGTCACGCC GGGCTCTACG TCCCAGGGAG      3540
GGAGGGGCGG CCCACACCCA GGCCCGCACC GCTGGGAGTC TGAGGCCTGA GTGAGTGTTT      3600
GGCCGAGGCC TGCATGTCCG GCTGAAGGCT GAGTGTCCGG CTGAGGCCTG AGCGAGTGTC      3660
CAGCCAAGGG CTGAGTGTCC AGCACACCTG CCGTCTTCAC TTCCCCACAG GCTGGCGCTC      3720
GGCTCCACCC CAGGGCCAGC TTTTCCTCAC CAGGAGCCCG GCTTCCACTC CCCACATAGG      3780
AATAGTCCAT CCCCTGAT                                     3798

```

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1154 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

His Ala Ser Gly Gln Arg Cys Val Leu Leu Arg Thr Trp Glu Ala Leu
1           5           10           15
Ala Pro Ala Thr Pro Ala Met Pro Arg Ala Pro Arg Cys Arg Ala Val
20           25           30
Arg Ser Leu Leu Arg Ser His Tyr Arg Glu Val Leu Pro Leu Ala Thr
35           40           45
Phe Val Arg Arg Leu Gly Pro Gln Gly Trp Arg Leu Val Gln Arg Gly
50           55           60
Asp Pro Ala Ala Phe Arg Ala Leu Val Ala Gln Cys Leu Val Cys Val
65           70           75           80
Pro Trp Asp Ala Arg Pro Pro Pro Ala Ala Pro Ser Phe Arg Gln Val
85           90           95
Ser Cys Leu Lys Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu
100          105          110
Arg Gly Ala Lys Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly
115          120          125
Ala Arg Gly Gly Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr
130          135          140

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Leu 145	Pro	Asn	Thr	Val	Thr 150	Asp	Ala	Leu	Arg	Gly 155	Ser	Gly	Ala	Trp	Gly 160
Leu	Leu	Leu	Arg	Arg 165	Val	Gly	Asp	Asp	Val 170	Leu	Val	His	Leu	Leu	Ala 175
Arg	Cys	Ala	Leu 180	Phe	Val	Leu	Val	Ala 185	Pro	Ser	Cys	Ala	Tyr 190	Gln	Val
Cys	Gly	Pro 195	Pro	Leu	Tyr	Gln	Leu 200	Gly	Ala	Ala	Thr	Gln 205	Ala	Arg	Pro
Pro	Pro 210	His	Ala	Ser	Gly	Pro 215	Arg	Arg	Arg	Leu	Gly 220	Cys	Glu	Arg	Ala
Trp 225	Asn	His	Ser	Val	Arg 230	Glu	Ala	Gly	Val	Pro 235	Leu	Gly	Leu	Pro	Ala 240
Pro	Gly	Ala	Arg	Arg 245	Arg	Gly	Gly	Ser	Ala 250	Ser	Arg	Ser	Leu	Pro 255	Leu
Pro	Lys	Arg	Pro 260	Arg	Arg	Gly	Ala	Ala 265	Pro	Glu	Pro	Glu	Arg 270	Thr	Pro
Val	Gly	Gln 275	Gly	Ser	Trp	Ala	His 280	Pro	Gly	Arg	Thr	Arg 285	Gly	Pro	Ser
Asp	Arg 290	Gly	Phe	Cys	Val	Val 295	Ser	Pro	Ala	Arg	Pro 300	Ala	Glu	Glu	Ala
Thr 305	Ser	Leu	Glu	Gly	Ala 310	Leu	Ser	Gly	Thr	Arg 315	His	Ser	His	Pro	Ser 320
Val	Gly	Arg	Gln	His 325	His	Ala	Gly	Pro	Pro 330	Ser	Thr	Ser	Arg	Pro 335	Pro
Arg	Pro	Trp	Asp 340	Thr	Pro	Cys	Pro	Pro 345	Val	Tyr	Ala	Glu	Thr 350	Lys	His
Phe	Leu	Tyr 355	Ser	Ser	Gly	Asp	Lys 360	Glu	Gln	Leu	Arg	Pro 365	Ser	Phe	Leu
Leu	Ser 370	Ser	Leu	Arg	Pro	Ser 375	Leu	Thr	Gly	Ala	Arg 380	Arg	Leu	Val	Glu
Thr 385	Ile	Phe	Leu	Gly	Ser 390	Arg	Pro	Trp	Met	Pro 395	Gly	Thr	Pro	Arg	Arg 400
Leu	Pro	Arg	Leu	Pro 405	Gln	Arg	Tyr	Trp	Gln 410	Met	Arg	Pro	Leu	Phe	Leu 415
Glu	Leu	Leu	Gly 420	Asn	His	Ala	Gln	Cys 425	Pro	Tyr	Gly	Val	Leu 430	Leu	Lys
Thr	His	Cys 435	Pro	Leu	Arg	Ala	Ala 440	Val	Thr	Pro	Ala	Ala 445	Gly	Val	Cys
Ala	Arg 450	Glu	Lys	Pro	Gln	Gly 455	Ser	Val	Ala	Ala	Pro 460	Glu	Glu	Glu	Asp
Thr 465	Asp	Pro	Arg	Arg	Leu 470	Val	Gln	Leu	Leu	Arg 475	Gln	His	Ser	Ser	Pro 480

Trp	Gln	Val	Tyr	Gly	Phe	Val	Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro
				485					490					495	
Pro	Gly	Leu	Trp	Gly	Ser	Arg	His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn
			500					505					510		
Thr	Lys	Lys	Phe	Ile	Ser	Leu	Gly	Lys	His	Ala	Lys	Leu	Ser	Leu	Gln
		515					520					525			
Glu	Leu	Thr	Trp	Lys	Met	Ser	Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg
	530					535					540				
Ser	Pro	Gly	Val	Gly	Cys	Val	Pro	Ala	Ala	Glu	His	Arg	Leu	Arg	Glu
545					550					555					560
Glu	Ile	Leu	Ala	Lys	Phe	Leu	His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val
				565					570					575	
Glu	Leu	Leu	Arg	Ser	Phe	Phe	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys
			580					585					590		
Asn	Arg	Leu	Phe	Phe	Tyr	Arg	Lys	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser
		595					600					605			
Ile	Gly	Ile	Arg	Gln	His	Leu	Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser
	610					615					620				
Glu	Ala	Glu	Val	Arg	Gln	His	Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu	Thr
625					630					635					640
Ser	Arg	Leu	Arg	Phe	Ile	Pro	Lys	Pro	Asp	Gly	Leu	Arg	Pro	Ile	Val
				645					650					655	
Asn	Met	Asp	Tyr	Val	Val	Gly	Ala	Arg	Thr	Phe	Arg	Arg	Glu	Lys	Arg
			660					665					670		
Ala	Glu	Arg	Leu	Thr	Ser	Arg	Val	Lys	Ala	Leu	Phe	Ser	Val	Leu	Asn
		675					680					685			
Tyr	Glu	Arg	Ala	Arg	Arg	Pro	Gly	Leu	Leu	Gly	Ala	Ser	Val	Leu	Gly
	690					695					700				
Leu	Asp	Asp	Ile	His	Arg	Ala	Trp	Arg	Thr	Phe	Val	Leu	Arg	Val	Arg
705					710					715					720
Ala	Gln	Asp	Pro	Pro	Pro	Glu	Leu	Tyr	Phe	Val	Lys	Val	Asp	Val	Thr
				725					730					735	
Gly	Ala	Tyr	Asp	Thr	Ile	Pro	Gln	Asp	Arg	Leu	Thr	Glu	Val	Ile	Ala
			740					745					750		
Ser	Ile	Ile	Lys	Pro	Gln	Asn	Thr	Tyr	Cys	Val	Arg	Arg	Tyr	Ala	Val
		755					760					765			
Val	Gln	Lys	Ala	Ala	His	Gly	His	Val	Arg	Lys	Ala	Phe	Lys	Ser	His
	770					775					780				
Val	Ser	Thr	Leu	Thr	Asp	Leu	Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala
785					790					795					800
His	Leu	Gln	Glu	Thr	Ser	Pro	Leu	Arg	Asp	Ala	Val	Val	Ile	Glu	Gln
				805					810					815	

Ser	Ser	Ser	Leu	Asn	Glu	Ala	Ser	Ser	Gly	Leu	Phe	Asp	Val	Phe	Leu			
			820					825					830					
Arg	Phe	Met	Cys	His	His	Ala	Val	Arg	Ile	Arg	Gly	Lys	Ser	Tyr	Val			
		835					840					845						
Gln	Cys	Gln	Gly	Ile	Pro	Gln	Gly	Ser	Ile	Leu	Ser	Thr	Leu	Leu	Cys			
	850					855					860							
Ser	Leu	Cys	Tyr	Gly	Asp	Met	Glu	Asn	Lys	Leu	Phe	Ala	Gly	Ile	Arg			
865					870					875					880			
Arg	Asp	Gly	Leu	Leu	Leu	Arg	Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr			
				885					890					895				
Pro	His	Leu	Thr	His	Ala	Lys	Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly			
			900					905					910					
Val	Pro	Glu	Tyr	Gly	Cys	Val	Val	Asn	Leu	Arg	Lys	Thr	Val	Val	Asn			
		915					920					925						
Phe	Pro	Val	Glu	Asp	Glu	Ala	Leu	Gly	Gly	Thr	Ala	Phe	Val	Gln	Met			
	930					935					940							
Pro	Ala	His	Gly	Leu	Phe	Pro	Trp	Cys	Gly	Leu	Leu	Leu	Asp	Thr	Arg			
945					950					955					960			
Thr	Leu	Glu	Val	Gln	Ser	Asp	Tyr	Ser	Ser	Tyr	Ala	Arg	Thr	Ser	Ile			
				965					970					975				
Arg	Ala	Ser	Leu	Thr	Phe	Asn	Arg	Gly	Phe	Lys	Ala	Gly	Arg	Asn	Met			
			980					985					990					
Arg	Arg	Lys	Leu	Phe	Gly	Val	Leu	Arg	Leu	Lys	Cys	His	Ser	Leu	Phe			
		995					1000					1005						
Leu	Asp	Leu	Gln	Val	Asn	Ser	Leu	Gln	Thr	Val	Cys	Thr	Asn	Ile	Tyr			
	1010					1015					1020							
Lys	Ile	Leu	Leu	Leu	Gln	Ala	Tyr	Arg	Phe	His	Ala	Cys	Val	Leu	Gln			
1025					1030					1035					1040			
Leu	Pro	Phe	His	Gln	Gln	Val	Trp	Lys	Asn	Pro	Thr	Phe	Phe	Leu	Arg			
				1045					1050					1055				
Val	Ile	Ser	Asp	Thr	Ala	Ser	Leu	Cys	Tyr	Ser	Ile	Leu	Lys	Ala	Lys			
			1060					1065					1070					
Asn	Ala	Gly	Met	Ser	Leu	Gly	Ala	Lys	Gly	Ala	Ala	Gly	Pro	Leu	Pro			
		1075					1080					1085						
Ser	Glu	Ala	Val	Gln	Trp	Leu	Cys	His	Gln	Ala	Phe	Leu	Leu	Lys	Leu			
	1090					1095					1100							
Thr	Arg	His	Arg	Val	Thr	Tyr	Val	Pro	Leu	Leu	Gly	Ser	Leu	Arg	Thr			
1105					1110						1115				1120			
Ala	Gln	Thr	Gln	Leu	Ser	Arg	Lys	Leu	Pro	Gly	Thr	Thr	Leu	Thr	Ala			
				1125					1130						1135			

Leu Glu Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile
 1140 1145 1150

Leu Asp

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligo nucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TGGATGATTT CTTGTTGGTG ACAC

24

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligo nucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AGCTTGGTAC CAACATGGAC TACAAGGACG ACGATG

36

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligo nucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AATTCCCTTG TCATCGTCGT CCTGTAGTC CATGTT

36

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligo nucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CGTTTGGTGG CTGATTTCTT GTTGGTGAC

29

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligo nucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTCACCAACA AGAAATCAGC CACCAAACG

29

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligo nucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GTCACCAACA AGAAAGCATC CACCAAACG

29

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligo nucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTCACCAACA AGAAAGCAGC CACCAAACG

29

- (2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligo nucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GAATTCTAGA TCACTTGTC TCGTCGTCCT TGTAGTCGTC CAGGATGGTC TTGAAGTC

58

- (2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligo nucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CGTTTGGTGG CTGATTTCTT GTTGGTGAC

29

- (2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligo nucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CGTTTGGTGG ATGCTTTCTT GTTGGTGAC

29

- (2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligo nucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CGTTTGGTGG CTGCTTTCTT GTTGGTGAC

29

- (2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ser	Glu	Ala	Glu	Val	Arg	Gln	His	Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu
1				5					10					15	

Thr	Ser	Arg	Leu	Arg	Phe	Ile	Pro	Lys	Cys
			20					25	

- (2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Arg	Ser	Lys	Arg	Arg	Ser	Arg	Gln	Pro	Pro	Arg	Pro	Gln	Lys	Thr	Glu
1				5					10					15	

Arg	Pro	Phe	Ser	Glu	Arg	Gly	Lys
							20

- (2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Asp Pro Asp Ala Ser Gly Thr Phe Arg Ser Cys Pro Pro Glu Ala Leu
 1 5 10 15

Lys Asp Leu

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligo nucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CCCGGGTGGC GGAGGTGGG C

21

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligo nucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CGACTTTGGA GGTGCCTTCA

20

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligo nucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GGGAAGCTTT AATACGACTC ACTATAGGGT GGCCTGGGA G

41

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligo nucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CCCGGGGGTT CACAAGCCCC C

21

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligo nucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GGGAAGCTTT AATACGACTC ACTATAGGGG GTTCACAAGC CCCC

44

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligo nucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCCGGGTGGG CCTGGGAG

18

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Arg Phe Ile Pro Lys
1 5

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Gly Ile Pro Gln Gly Ser
1 5

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu
1 5 10